

SEQUENCE LISTING

<110> WUCHERPFENNIG, Kai W
STROMINGER, Jack L

<120> MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING
DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES
THEREFOR

<130> HAR-005

<140> 09/248,964
<141> 1999-02-12

<150> PCT/US97/14503
<151> 1997-08-15

<150> 60/075,351
<151> 1998-02-19

<150> 60/024,007
<151> 1996-08-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1
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<223> Description of Artificial Sequence: DR2-Fos fusion

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<220>
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<223> 3' end of secretory signal

<220>
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<222> (22)..(594)
<223> DRA*0101 extracellular domain

<220>
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<222> (595)..(615)
<223> Linker sequence

<220>
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<222> (616)..(735)
<223> Fos leucine zipper domain



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<400> 1

| | |
|---|-----|
| gta tct ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag | 48 |
| Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln | |
| 1 5 10 15 | |
| gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac | 96 |
| Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp | |
| 20 25 30 | |
| ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg | 144 |
| Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr | |
| 35 40 45 | |
| gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa | 192 |
| Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln | |
| 50 55 60 | |
| ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg | 240 |
| Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met | |
| 65 70 75 80 | |
| aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta | 288 |
| Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val | |
| 85 90 95 | |
| act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc | 336 |
| Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu | |
| 100 105 110 | |
| atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg | 384 |
| Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp | |
| 115 120 125 | |
| ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc | 432 |
| Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe | |
| 130 135 140 | |
| ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc | 480 |
| Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe | |
| 145 150 155 160 | |
| ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc | 528 |
| Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly | |
| 165 170 175 | |
| ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct | 576 |
| Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro | |
| 180 185 190 | |
| ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat | 624 |
| Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp | |
| 195 200 205 | |
| aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg | 672 |
| Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu | |
| 210 215 220 | |

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cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc 720
 Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
 225 230 235 240

atc ctg gcc gcc cat tgagaattct atgac 750
 Ile Leu Ala Ala His
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<210> 2
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 <223> Description of Artificial Sequence: DR2-Fos fusion

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 <223> 3' end of secretory signal

<220>
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 <222> (8)..(198)
 <223> DRA*0101 extracellular domain

<220>
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 <222> (199)..(205)
 <223> Linker sequence

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 <222> (206)..(245)
 <223> Fos leucine zipper domain

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Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
 20 25 30

Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
 35 40 45

Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
 50 55 60

Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
 65 70 75 80

Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
 85 90 95

Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
 100 105 110

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Cys | Phe | Ile | Asp | Lys | Phe | Thr | Pro | Pro | Val | Val | Asn | Val | Thr | Trp |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| | | | | | | | | | | | | | | | |
| Leu | Arg | Asn | Gly | Lys | Pro | Val | Thr | Thr | Gly | Val | Ser | Glu | Thr | Val | Phe |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| | | | | | | | | | | | | | | | |
| Leu | Pro | Arg | Glu | Asp | His | Leu | Phe | Arg | Lys | Phe | His | Tyr | Leu | Pro | Phe |
| | | 145 | | | 150 | | | | | 155 | | | | | 160 |
| | | | | | | | | | | | | | | | |
| Leu | Pro | Ser | Thr | Glu | Asp | Val | Tyr | Asp | Cys | Arg | Val | Glu | His | Trp | Gly |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| | | | | | | | | | | | | | | | |
| Leu | Asp | Glu | Pro | Leu | Leu | Lys | His | Trp | Glu | Phe | Asp | Ala | Pro | Ser | Pro |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| | | | | | | | | | | | | | | | |
| Leu | Pro | Glu | Thr | Thr | Glu | Val | Asp | Gly | Gly | Gly | Gly | Gly | Leu | Thr | Asp |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| | | | | | | | | | | | | | | | |
| Thr | Leu | Gln | Ala | Glu | Thr | Asp | Gln | Leu | Glu | Asp | Glu | Lys | Ser | Ala | Leu |
| | | 210 | | | | 215 | | | | | 220 | | | | |
| | | | | | | | | | | | | | | | |
| Gln | Thr | Glu | Ile | Ala | Asn | Leu | Leu | Lys | Glu | Lys | Glu | Lys | Leu | Glu | Phe |
| | | 225 | | | 230 | | | | | 235 | | | | | 240 |
| | | | | | | | | | | | | | | | |
| Ile | Leu | Ala | Ala | His | | | | | | | | | | | |
| | | | | 245 | | | | | | | | | | | |

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<223> Description of Artificial Sequence: DR2-Jun fusion

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<222> (22)..(615)

<223> DRB1*1501 extracellular domain

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<221> misc_feature

<222> (616)..(636)

<223> Linker sequence

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<222> (637)..(756)

<223> Jun leucine zipper domain

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| gta tct ctc gag aaa aga gag ggg gac acc cga cca cgt ttc ctg tgg | 48 |
| Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp | |
| 1 5 10 15 | |
| cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg | 96 |
| Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg | |
| 20 25 30 | |
| ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac | 144 |
| Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp | |
| 35 40 45 | |
| agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac | 192 |
| Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp | |
| 50 55 60 | |
| gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cgg gcc | 240 |
| Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala | |
| 65 70 75 80 | |
| gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc | 288 |
| Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe | |
| 85 90 95 | |
| aca gtg cag cgg cga gtc caa cct aag gtg act gta tat cct tca aag | 336 |
| Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys | |
| 100 105 110 | |
| acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt | 384 |
| Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly | |
| 115 120 125 | |
| ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa | 432 |
| Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu | |
| 130 135 140 | |
| gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg | 480 |
| Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp | |
| 145 150 155 160 | |
| acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag | 528 |
| Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu | |
| 165 170 175 | |
| gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca | 576 |
| Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr | |
| 180 185 190 | |
| gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga | 624 |
| Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly | |
| 195 200 205 | |

ggt ggc ggc ggt cgc atc gcc cgg ctc gag gaa aaa gtg aaa acc ttg 672
 Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
 210 215 220

aaa gct cag aac tcg gag ctc gcg tcc acg gcc aac atg ctc agg gaa 720
 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
 225 230 235 240

cag gtg gca cag ctt aaa cag aaa gtc atg aac cat tgagaattct atgac 771
 Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
 245 250

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 <223> DRB1*1501 extracellular domain

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 <222> (206)..(212)
 <223> Linker sequence

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 <222> (213)..(252)
 <223> Jun leucine zipper domain

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 Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp
 1 5 10 15

Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
 20 25 30

Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
 35 40 45

Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
 50 55 60

Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
 65 70 75 80

Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
85 90 95

Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
100 105 110

Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
115 120 125

Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
130 135 140

Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
145 150 155 160

Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
165 170 175

Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
180 185 190

Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
195 200 205

Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
210 215 220

Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
225 230 235 240

Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
245 250

<210> 5
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

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gtatctctcg agaaaagaga gatcaaagaa gaacatgtga tc

42

<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 6
gtcatagaat tctcaatggg cggccaggat gaactccag

39

<210> 7
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 7
gtatctctcg agaaaagaga gggggacacc cgaccacgtt tc 42

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 8
gtcatagaat tctcaatggt tcatgacttt ctgtttaag 39

<210> 9
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic,
biotin ligase recognition sequence

<400> 9
Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp
1 5 10

<210> 10
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic,
linker sequence

<400> 10
Ser Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 11
<211> 1446

<212> DNA
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<223> Linker

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<223> Fos leucine zipper domain

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<222> (730)..(1437)
<223> IgG domain

<400> 11
ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag gcc gag 48
Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu
1 5 10 15

ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac ttt gat 96
Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
20 25 30

ggg gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg 144
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45

cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca 192
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60

ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg aca aag 240
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cg | tc | aa | ta | ac | cc | at | ac | aa | gt | cc | cc | ga | gt | ac | gt | 288 |
| Arg | Ser | Asn | Tyr | Thr | Pro | Ile | Thr | Asn | Val | Pro | Pro | Glu | Val | Thr | Val | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| ct | ac | aa | ag | cc | gt | ga | ct | ag | ga | cc | aa | gt | ct | at | tg | 336 |
| Leu | Thr | Asn | Ser | Pro | Val | Glu | Leu | Arg | Glu | Pro | Asn | Val | Leu | Ile | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| tt | at | ga | aa | tt | ac | cc | cc | gt | gt | aa | gt | ac | tg | ct | cg | 384 |
| Phe | Ile | Asp | Lys | Phe | Thr | Pro | Pro | Val | Val | Asn | Val | Thr | Trp | Leu | Arg | |
| | | 115 | | | | | | 120 | | | | 125 | | | | |
| aa | gg | aa | cc | gt | ac | aa | gg | gt | tc | ga | aa | gt | tt | ct | cc | 432 |
| Asn | Gly | Lys | Pro | Val | Thr | Thr | Gly | Val | Ser | Glu | Thr | Val | Phe | Leu | Pro | |
| | 130 | | | | | | 135 | | | | | 140 | | | | |
| ag | ga | ga | ca | ct | tt | cg | aa | tt | ca | ta | ct | cc | tt | ct | cc | 480 |
| Arg | Glu | Asp | His | Leu | Phe | Arg | Lys | Phe | His | Tyr | Leu | Pro | Phe | Leu | Pro | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| tc | ac | ga | ga | gt | ta | ga | tg | ag | gt | ga | ca | tg | gg | tg | ga | 528 |
| Ser | Thr | Glu | Asp | Val | Tyr | Asp | Cys | Arg | Val | Glu | His | Trp | Gly | Leu | Asp | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| ga | cc | ct | ct | aa | ca | tg | ga | tt | ga | gc | cc | ag | cc | ct | cc | 576 |
| Glu | Pro | Leu | Leu | Lys | His | Trp | Glu | Phe | Asp | Ala | Pro | Ser | Pro | Leu | Pro | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| ga | ac | aa | ga | gt | ga | gg | gg | gg | gg | gg | ta | ac | ga | aa | ct | 624 |
| Glu | Thr | Thr | Glu | Val | Asp | Gly | Gly | Gly | Gly | Gly | Leu | Thr | Asp | Thr | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| ca | gc | ga | aa | ga | ca | ct | ga | ga | ga | aa | tc | gc | tg | ca | ac | 672 |
| Gln | Ala | Glu | Thr | Asp | Gln | Leu | Glu | Asp | Glu | Lys | Ser | Ala | Leu | Gln | Thr | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| ga | at | gc | aa | ca | ct | aa | ga | aa | ga | aa | ct | ga | tt | at | ct | 720 |
| Glu | Ile | Ala | Asn | Leu | Leu | Lys | Glu | Lys | Glu | Lys | Leu | Glu | Phe | Ile | Leu | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| gc | gc | ca | ga | ga | tc | ga | cc | ga | gg | cc | aa | at | aa | cc | tg | 768 |
| Ala | Ala | His | Ala | Ala | Ser | Glu | Pro | Arg | Gly | Pro | Thr | Ile | Lys | Pro | Cys | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| cc | cc | tg | aa | tg | cc | ga | cc | aa | ct | tt | gg | gg | cc | tc | gt | 816 |
| Pro | Pro | Cys | Lys | Cys | Pro | Ala | Pro | Asn | Leu | Leu | Gly | Gly | Pro | Ser | Val | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| tt | at | tt | cc | cc | aa | at | aa | ga | gt | ct | at | at | tc | ct | ag | 864 |
| Phe | Ile | Phe | Pro | Pro | Lys | Ile | Lys | Asp | Val | Leu | Met | Ile | Ser | Leu | Ser | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| cc | at | gt | aa | tg | gt | gt | gt | ga | gt | ag | ga | ga | ga | cc | ga | 912 |
| Pro | Ile | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | Glu | Asp | Asp | Pro | Asp | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |

| | |
|---|------|
| gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag | 960 |
| Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln | |
| 305 310 315 320 | |
| aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt | 1008 |
| Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser | |
| 325 330 335 | |
| gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa | 1056 |
| Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys | |
| 340 345 350 | |
| tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc | 1104 |
| Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile | |
| 355 360 365 | |
| tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct | 1152 |
| Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro | |
| 370 375 380 | |
| cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg | 1200 |
| Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met | |
| 385 390 395 400 | |
| gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac | 1248 |
| Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn | |
| 405 410 415 | |
| ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct | 1296 |
| Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser | |
| 420 425 430 | |
| gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac | 1344 |
| Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn | |
| 435 440 445 | |
| tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg | 1392 |
| Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu | |
| 450 455 460 | |
| cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aaa | 1437 |
| His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys | |
| 465 470 475 | |
| tgagaattc | 1446 |

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<223> Description of Artificial Sequence: DR2-IgG fusion

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<221> misc_feature

<222> (1)..(5)
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<222> (6)..(196)
<223> DRA*0101 extracellular domain

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<223> Fos leucine zipper domain

<220>
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<222> (244)..(479)
<223> IgG domain

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Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu
1 5 10 15
Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
20 25 30
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80
Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
85 90 95
Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
100 105 110
Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
115 120 125
Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
130 135 140
Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145 150 155 160
Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 165 | | | | | | | 170 | | | | | | 175 | | | |
| Glu | Pro | Leu | Leu | Lys | His | Trp | Glu | Phe | Asp | Ala | Pro | Ser | Pro | Leu | Pro | |
| | | | 180 | | | | 185 | | | | | | 190 | | | |
| Glu | Thr | Thr | Glu | Val | Asp | Gly | Gly | Gly | Gly | Gly | Leu | Thr | Asp | Thr | Leu | |
| | | 195 | | | | 200 | | | | | | 205 | | | | |
| Gln | Ala | Glu | Thr | Asp | Gln | Leu | Glu | Asp | Glu | Lys | Ser | Ala | Leu | Gln | Thr | |
| | | 210 | | | | 215 | | | | 220 | | | | | | |
| Glu | Ile | Ala | Asn | Leu | Leu | Lys | Glu | Lys | Glu | Lys | Leu | Glu | Phe | Ile | Leu | |
| 225 | | | | 230 | | | | | | 235 | | | 240 | | | |
| Ala | Ala | His | Ala | Ala | Ser | Glu | Pro | Arg | Gly | Pro | Thr | Ile | Lys | Pro | Cys | |
| | | | 245 | | | | | | 250 | | | 255 | | | | |
| Pro | Pro | Cys | Lys | Cys | Pro | Ala | Pro | Asn | Leu | Leu | Gly | Gly | Pro | Ser | Val | |
| | | 260 | | | | | | 265 | | | 270 | | | | | |
| Phe | Ile | Phe | Pro | Pro | Lys | Ile | Lys | Asp | Val | Leu | Met | Ile | Ser | Leu | Ser | |
| | | 275 | | | | | | 280 | | | 285 | | | | | |
| Pro | Ile | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | Glu | Asp | Asp | Pro | Asp | |
| | | 290 | | | 295 | | | | | | 300 | | | | | |
| Val | Gln | Ile | Ser | Trp | Phe | Val | Asn | Asn | Val | Glu | Val | His | Thr | Ala | Gln | |
| 305 | | | | 310 | | | | | | 315 | | | 320 | | | |
| Thr | Gln | Thr | His | Arg | Glu | Asp | Tyr | Asn | Ser | Thr | Leu | Arg | Val | Val | Ser | |
| | | | 325 | | | | | | 330 | | | 335 | | | | |
| Ala | Leu | Pro | Ile | Gln | His | Gln | Asp | Trp | Met | Ser | Gly | Lys | Glu | Phe | Lys | |
| | | 340 | | | | | | 345 | | | 350 | | | | | |
| Cys | Lys | Val | Asn | Asn | Lys | Asp | Leu | Pro | Ala | Pro | Ile | Glu | Arg | Thr | Ile | |
| | | 355 | | | | | | 360 | | | 365 | | | | | |
| Ser | Lys | Pro | Lys | Gly | Ser | Val | Arg | Ala | Pro | Gln | Val | Tyr | Val | Leu | Pro | |
| | | 370 | | | 375 | | | | | | 380 | | | | | |
| Pro | Pro | Glu | Glu | Glu | Met | Thr | Lys | Lys | Gln | Val | Thr | Leu | Thr | Cys | Met | |
| 385 | | | | 390 | | | | | | 395 | | | 400 | | | |
| Val | Thr | Asp | Phe | Met | Pro | Glu | Asp | Ile | Tyr | Val | Glu | Trp | Thr | Asn | Asn | |
| | | | 405 | | | | | | 410 | | | 415 | | | | |
| Gly | Lys | Thr | Glu | Leu | Asn | Tyr | Lys | Asn | Thr | Glu | Pro | Val | Leu | Asp | Ser | |
| | | 420 | | | | | | 425 | | | 430 | | | | | |
| Asp | Gly | Ser | Tyr | Phe | Met | Tyr | Ser | Lys | Leu | Arg | Val | Glu | Lys | Lys | Asn | |
| | | 435 | | | | | | 440 | | | 445 | | | | | |
| Trp | Val | Glu | Arg | Asn | Ser | Tyr | Ser | Cys | Ser | Val | Val | His | Glu | Gly | Leu | |
| | | 450 | | | 455 | | | | | | 460 | | | | | |
| His | Asn | His | His | Thr | Thr | Lys | Ser | Phe | Ser | Arg | Thr | Pro | Gly | Lys | | |

465

470

475

<210> 13

<211> 1851

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-IgM fusion

<220>

<221> CDS

<222> (1)..(1836)

<220>

<221> misc_feature

<222> (1)..(75)

<223> 3' end of secretory signal

<220>

<221> misc_feature

<222> (76)..(648)

<223> DRA*0101 extracellular domain

<220>

<221> misc_feature

<222> (649)..(669)

<223> Linker

<220>

<221> misc_feature

<222> (670)..(789)

<223> Fos leucine zipper domain

<220>

<221> misc_feature

<222> (790)..(1836)

<223> IgG domain

<400> 13

atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg 48

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val

1

5

10

15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96

Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile

20

25

30

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg 144

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met

35

40

45

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag 192

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys

50

55

60

| | |
|---|-----|
| gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag | 240 |
| Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu | |
| 65 70 75 80 | |
| gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa | 288 |
| Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu | |
| 85 90 95 | |
| atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca | 336 |
| Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro | |
| 100 105 110 | |
| gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac | 384 |
| Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn | |
| 115 120 125 | |
| gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc | 432 |
| Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val | |
| 130 135 140 | |
| acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca | 480 |
| Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr | |
| 145 150 155 160 | |
| gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc | 528 |
| Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu | |
| 165 170 175 | |
| ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac | 576 |
| Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His | |
| 180 185 190 | |
| tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca | 624 |
| Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro | |
| 195 200 205 | |
| agc cct ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta | 672 |
| Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu | |
| 210 215 220 | |
| act gat aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct | 720 |
| Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser | |
| 225 230 235 240 | |
| gcg ttg cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg | 768 |
| Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu | |
| 245 250 255 | |
| gag ttc atc ctg gcc gcc cac gtc gca gaa atg aac ccc aat gta aat | 816 |
| Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn | |
| 260 265 270 | |
| gtg ttc gtc cca cca cgg gat ggc ttc tct ggc cct gca cca cgc aag | 864 |
| Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys | |
| 275 280 285 | |
| tct aaa ctc atc tgc gag gcc acg aac ttc act cca aaa ccg atc aca | 912 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Ser | Lys | Leu | Ile | Cys | Glu | Ala | Thr | Asn | Phe | Thr | Pro | Lys | Pro | Ile | Thr | | |
| 290 | | | | | | 295 | | | | | 300 | | | | | | |
| gta | tcc | tgg | cta | aag | gat | ggg | aag | ctc | gtg | gaa | tct | ggc | ttc | acc | aca | 960 | |
| Val | Ser | Trp | Leu | Lys | Asp | Gly | Lys | Leu | Val | Glu | Ser | Gly | Phe | Thr | Thr | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| gat | ccg | gtg | acc | atc | gag | aac | aaa | gga | tcc | aca | ccc | caa | acc | tac | aag | 1008 | |
| Asp | Pro | Val | Thr | Ile | Glu | Asn | Lys | Gly | Ser | Thr | Pro | Gln | Thr | Tyr | Lys | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| gtc | ata | agc | aca | ctt | acc | atc | tct | gaa | atc | gac | tgg | ctg | aac | ctg | aat | 1056 | |
| Val | Ile | Ser | Thr | Leu | Thr | Ile | Ser | Glu | Ile | Asp | Trp | Leu | Asn | Leu | Asn | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| gtg | tac | acc | tgc | cgt | gtg | gat | cac | agg | ggg | ctc | acc | ttc | ttg | aag | aac | 1104 | |
| Val | Tyr | Thr | Cys | Arg | Val | Asp | His | Arg | Gly | Leu | Thr | Phe | Leu | Lys | Asn | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| gtg | tcc | tcc | aca | tgt | gct | gcc | agt | ccc | tcc | aca | gat | atc | ctt | aat | ttt | 1152 | |
| Val | Ser | Ser | Thr | Cys | Ala | Ala | Ser | Pro | Ser | Thr | Asp | Ile | Leu | Asn | Phe | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |
| act | att | cct | cct | tcc | ttt | gcc | gac | atc | ttc | ctt | agc | aag | tcc | gct | aac | 1200 | |
| Thr | Ile | Pro | Pro | Ser | Phe | Ala | Asp | Ile | Phe | Leu | Ser | Lys | Ser | Ala | Asn | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | |
| ctg | acc | tgt | ctg | gtc | tca | aac | ctg | gca | acc | tat | gaa | acc | ctg | agt | atc | 1248 | |
| Leu | Thr | Cys | Leu | Val | Ser | Asn | Leu | Ala | Thr | Tyr | Glu | Thr | Leu | Ser | Ile | | |
| | | | | 405 | | | | | 410 | | | | | | 415 | | |
| tcc | tgg | gct | tct | caa | agt | ggg | gaa | cca | ctg | gaa | acc | aaa | att | aaa | atc | 1296 | |
| Ser | Trp | Ala | Ser | Gln | Ser | Gly | Glu | Pro | Leu | Glu | Thr | Lys | Ile | Lys | Ile | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| atg | gaa | agc | cat | ccc | aat | ggc | acc | ttc | agt | gct | aag | ggg | gtg | gct | agt | 1344 | |
| Met | Glu | Ser | His | Pro | Asn | Gly | Thr | Phe | Ser | Ala | Lys | Gly | Val | Ala | Ser | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | |
| gtt | tgt | gtg | gaa | gac | tgg | aat | aac | agg | aag | gaa | ttt | gtg | tgt | act | gtg | 1392 | |
| Val | Cys | Val | Glu | Asp | Trp | Asn | Asn | Arg | Lys | Glu | Phe | Val | Cys | Thr | Val | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | | |
| act | cac | agg | gat | ctg | cct | tca | cca | cag | aag | aaa | ttc | atc | tca | aaa | ccc | 1440 | |
| Thr | His | Arg | Asp | Leu | Pro | Ser | Pro | Gln | Lys | Lys | Phe | Ile | Ser | Lys | Pro | | |
| 465 | | | | | 470 | | | | | | 475 | | | | 480 | | |
| aat | gag | gtg | cac | aaa | cat | cca | cct | gct | gtg | tac | ctg | ctg | cca | cca | gct | 1488 | |
| Asn | Glu | Val | His | Lys | His | Pro | Pro | Ala | Val | Tyr | Leu | Leu | Pro | Pro | Ala | | |
| | | | | 485 | | | | | 490 | | | | | 495 | | | |
| cgt | gaa | caa | ctg | aac | ctg | agg | gag | tca | gcc | aca | gtc | acc | tgc | ctg | gtg | 1536 | |
| Arg | Glu | Gln | Leu | Asn | Leu | Arg | Glu | Ser | Ala | Thr | Val | Thr | Cys | Leu | Val | | |
| | | | 500 | | | | | 505 | | | | | 510 | | | | |
| aag | ggc | ttc | tct | cct | gca | gac | atc | tct | gtg | caa | tgg | aag | cag | agg | ggc | 1584 | |
| Lys | Gly | Phe | Ser | Pro | Ala | Asp | Ile | Ser | Val | Gln | Trp | Lys | Gln | Arg | Gly | | |

| | | | |
|---|-----|-----|------|
| 515 | 520 | 525 | |
| cag ctc tta ccc cag gag aag tat gtg acc agt gcc ccg atg cca gag | | | 1632 |
| Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu | | | |
| 530 | 535 | 540 | |
| cct ggg gcc cca ggc ttc tac ttt acc cac agc atc ctg act gtg aca | | | 1680 |
| Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr | | | |
| 545 | 550 | 555 | 560 |
| gag gag gaa tgg aac tcc gga gag acc tat acc tgt gtt gta ggc cac | | | 1728 |
| Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His | | | |
| | 565 | 570 | 575 |
| gag gcc ctg cca cac ctg gtg acc gag agg acc gtg gac aag tcc act | | | 1776 |
| Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr | | | |
| | 580 | 585 | 590 |
| ggt aaa ccc aca ctg tac aat gtc tcc ctg atc atg tct gac aca ggc | | | 1824 |
| Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly | | | |
| | 595 | 600 | 605 |
| ggc acc tgc tat tgaagatctg togac | | | 1851 |
| Gly Thr Cys Tyr | | | |
| 610 | | | |

<210> 14
 <211> 612
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DR2-IgM fusion

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 <222> (1)..(25)
 <223> 3' end of secretory signal

<220>
 <221> misc_feature
 <222> (26)..(216)
 <223> DRA*0101 extracellular domain

<220>
 <221> misc_feature
 <222> (217)..(223)
 <223> Linker

<220>
 <221> misc_feature
 <222> (224)..(263)
 <223> Fos leucine zipper domain

<220>
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 <222> (264)..(612)

<223> IgG domain

<400> 14

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
1 5 10 15

Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
20 25 30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
35 40 45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
50 55 60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65 70 75 80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
85 90 95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
100 105 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
115 120 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145 150 155 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
165 170 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
180 185 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195 200 205

Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu
210 215 220

Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
225 230 235 240

Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
245 250 255

Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn
260 265 270

Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys
275 280 285

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Leu | Ile | Cys | Glu | Ala | Thr | Asn | Phe | Thr | Pro | Lys | Pro | Ile | Thr | 290 | 295 | 300 |
| Val | Ser | Trp | Leu | Lys | Asp | Gly | Lys | Leu | Val | Glu | Ser | Gly | Phe | Thr | Thr | 305 | 310 | 315 |
| Asp | Pro | Val | Thr | Ile | Glu | Asn | Lys | Gly | Ser | Thr | Pro | Gln | Thr | Tyr | Lys | 325 | 330 | 335 |
| Val | Ile | Ser | Thr | Leu | Thr | Ile | Ser | Glu | Ile | Asp | Trp | Leu | Asn | Leu | Asn | 340 | 345 | 350 |
| Val | Tyr | Thr | Cys | Arg | Val | Asp | His | Arg | Gly | Leu | Thr | Phe | Leu | Lys | Asn | 355 | 360 | 365 |
| Val | Ser | Ser | Thr | Cys | Ala | Ala | Ser | Pro | Ser | Thr | Asp | Ile | Leu | Asn | Phe | 370 | 375 | 380 |
| Thr | Ile | Pro | Pro | Ser | Phe | Ala | Asp | Ile | Phe | Leu | Ser | Lys | Ser | Ala | Asn | 385 | 390 | 395 |
| Leu | Thr | Cys | Leu | Val | Ser | Asn | Leu | Ala | Thr | Tyr | Glu | Thr | Leu | Ser | Ile | 405 | 410 | 415 |
| Ser | Trp | Ala | Ser | Gln | Ser | Gly | Glu | Pro | Leu | Glu | Thr | Lys | Ile | Lys | Ile | 420 | 425 | 430 |
| Met | Glu | Ser | His | Pro | Asn | Gly | Thr | Phe | Ser | Ala | Lys | Gly | Val | Ala | Ser | 435 | 440 | 445 |
| Val | Cys | Val | Glu | Asp | Trp | Asn | Asn | Arg | Lys | Glu | Phe | Val | Cys | Thr | Val | 450 | 455 | 460 |
| Thr | His | Arg | Asp | Leu | Pro | Ser | Pro | Gln | Lys | Lys | Phe | Ile | Ser | Lys | Pro | 465 | 470 | 475 |
| Asn | Glu | Val | His | Lys | His | Pro | Pro | Ala | Val | Tyr | Leu | Leu | Pro | Pro | Ala | 485 | 490 | 495 |
| Arg | Glu | Gln | Leu | Asn | Leu | Arg | Glu | Ser | Ala | Thr | Val | Thr | Cys | Leu | Val | 500 | 505 | 510 |
| Lys | Gly | Phe | Ser | Pro | Ala | Asp | Ile | Ser | Val | Gln | Trp | Lys | Gln | Arg | Gly | 515 | 520 | 525 |
| Gln | Leu | Leu | Pro | Gln | Glu | Lys | Tyr | Val | Thr | Ser | Ala | Pro | Met | Pro | Glu | 530 | 535 | 540 |
| Pro | Gly | Ala | Pro | Gly | Phe | Tyr | Phe | Thr | His | Ser | Ile | Leu | Thr | Val | Thr | 545 | 550 | 555 |
| Glu | Glu | Glu | Trp | Asn | Ser | Gly | Glu | Thr | Tyr | Thr | Cys | Val | Val | Gly | His | 565 | 570 | 575 |
| Glu | Ala | Leu | Pro | His | Leu | Val | Thr | Glu | Arg | Thr | Val | Asp | Lys | Ser | Thr | 580 | 585 | 590 |

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

Gly Thr Cys Tyr
610